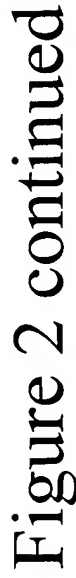


Figure 2

g1244708	1	-----MKSFCDNDNNHSTNTT	40
GmANT1	1	-----MKRINESNTDGNHNNH	31
OsANT2	1	-----MASGNSSSSGSMAATAG	48
GhANT1	1	-----MSNMGFSUTP-----	28
GmANT2	1	-----MKSMENDDADLNQNNH	63
OsANT1	1	-----MASGGSSNMGFSUTP	45
g1244708	41	-----SSSTSSAATSSSVPPQ	85
GmANT1	32	-----TSATATVPTTFYMSPSQ	71
OsANT2	49	-----HHVHQHQHQHGGGLFN	99
GhANT1	29	-----GLEAENVGLYSALP-----	30
GmANT2	64	-----AAAAAGAMSSPP-----	78
OsANT1	46	-----DSATTNCFLESPPAQ	103
g1244708	86	-----MPURSDGSLCIMEALNRS	125
GmANT1	72	-----MPUKSDGSLCILEALKRS	113
OsANT2	100	-----MPUKSDGSLCIMEALRG	137
GhANT1	31	-----MPURSDGSLCVCWDPFR	98
GmANT2	79	-----MPUKSDGSLYLETLRS	133
OsANT1	104	-----MPUKSDGSLCIMEGMP	131
g1244708	126	-----NTSHKEAMDLSLDFLN	159
GmANT1	114	-----HEYGSHERGLSDSYNS	158
OsANT2	138	-----AGPAMALSDNSAEYY	177
GhANT1	99	-----QNTVPSPTRINNVNAPNY	152
GmANT2	134	-----LSLDSVFYTIQPSRDPNN	188
OsANT1	132	-----CGNGSGHDPATYSSQ	165
g1244708	160	-----FPQTRNHEEETRN-YG	205
GmANT1	159	-----HPYYSGLACHGLYQAPL	226
OsANT2	178	-----GGFLQCAVTPGAGAG--	228
GhANT1	153	-----HSLQQCDPNPNHNR--	201
GmANT2	189	-----GSKQSDTSDNNLHVQNM	245
OsANT1	166	-----YNYQPLTEAEMLQEA	219
g1244708	206	-----QSSCITGSHHHQNNQ	272
GmANT1	227	-----ERNVSLGSGGELQSL	287
OsANT2	229	-----CAAGPIIPTGGHLPLTL	294
GhANT1	202	-----ETNNNFNGLSLTMS--	252
GmANT2	246	-----ESGSGMAYGDLQSL	309
OsANT1	220	-----GSQSSSCVSAAPQQH	280





g1244708	273	SUOTFGQRTSQYRGVTRHRWTRGRYEAHUWJNSFKKEGHSRKGRQVYLGGYDMEKKAARAYDLAALKYW	340	
GmANT1	288	SUOTFGQRTSQYRGVTRHRWTRGRYEAHUWJNSCKKEGQTRKGRQVYLGGYDMEKKAARAYDLAALKYW	355	
OsANT2	295	SUOTFGQRTSQYRGVTRHRWTRGRYEAHUWJNSCKKEGQTRKGRQVYLGGYDMEKKAARAYDLAALKYW	362	
GhANT1	253	SUOTFGQRTSQYRGVTRHRWTRGRYEAHUWJNSCKKEGQTRKGRQVYLGGYDMEKKAARAYDLAALKYW	320	
GmANT2	310	SUOTFGQRTSQYRGVTRHRWTRGRYEAHUWJNSCKKEGQTRKGRQVYLGGYDMEKKAARAYDLAALKYW	377	
OsANT1	281	SUOTFGQRTSQYRGVTRHRWTRGRYEAHUWJNSCKKEGQTRKGRQVYLGGYDTEKKAARAYDLAALKYW	348	
g1244708	341	GPSTHINFSAENYQKEDMKNMURQEYVAHLRRKSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGN	408	
	356	GPSTHINFSTENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGN	423	
	GmANT1	363	GPSTHINFPLEDYQEFLEEMKNMSRQEYVAHLRRKSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGN	430
	ZmANT1	1	-----LRRKSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGN	37
	GhANT1	321	GPSTHINFPLESTYEKLEEMKNMURQEFVAHLRRKSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGN	388
g1244708	378	GPSTHINFPLENYQNELEEMKNMURQEYVAHLRRKSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGN	445	
	GmANT2	349	GLSTHINFPLENYRDEEMERMURQEYVAHLRRRSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGN	416
g1244708	409	KDLYLGTG-----TQEEAAEAYDVAAIKFRGCTNAVTNFDIURYDVDRIMSSNLLSGE	462	
	GmANT1	424	KDLYLGTG-----TQEEAAEAYDVAAIKFRGANVTNFDIURYDVDRIMASSNLLAGE	477
	OsANT2	431	KDLYLGTGFIASFAARRARHAGITQEEAAEAYDVAAIKFRGLNAVTFNFDIURYDVDRIMASSNLLPGE	498
	ZmANT1	38	KDLYLGTGFS-----TQEEAAEAYDVAAIKFRGLSAVTNFDIURYDVDRIMASSNLLPGE	91
	GhANT1	389	KDLYLGTGFS-----TQEEAAEAYDVAAIKFRGTSAVTNFDIURYDVDRIMASSNLLIGGE	442
g1244708	446	KDLYLGTGFS-----TQEEAAEAYDVAAIKFRGANVTNFDIURYDVDRIMASSNLLSSE	499	
	GmANT2	417	KDLYLGTGFS-----TQEEAAEAYDVAAIKFRGLNAVTFNFDIURYDVDRIMASSNLLPGE	470
g1244708	463	LARR-----LARR-----NNNS-----LVRN-----	475	
	GmANT1	478	LARRKKONDPRNKDIDYKSWATSUNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQQANGSGDQK	545
	OsANT2	499	LARRKKGKVG-----DGGAARAVADAAALVQAGNV-----AEWKMATAAALPAARARTEQQQHG	553
	ZmANT1	92	QVRR-----KGDARAVSEAAALVQAGNC-----MTDTWKTQAAALPAARAR-----GAGQ	141
	GhANT1	443	LAKRSP-----KOTASIPEDYNSSCASSAPQLLAIPSGASDELADMVWTAN-----SDEQ	495
g1244708	500	LARRNRETNETQCIDQNHKPSAYEDTQEAILMHQKCESENDEWKMVLVYQSSQQLEQNPTIESDR	567	
	GmANT2	471	ARRKVAIEAAPDHVPIGR-ELGATEEASAAATV-----GTD-WRPMVLHGSQQQQQAACTEATADL	529
g1244708	476	-----TEDQTALNAVVEG-----GSKKEYSTUPE-R-----	499	
	GmANT1	546	IMNCGNYRNSAFSMALQDLTGIDSVSGQHMLDESSKI-GTHFSNTSS-LVTSLSGGRASPEKRG	611
	OsANT2	554	GGHQHDLPLSDAFSVLQDITVTDVDAAGAPPRAPHMSMAAT-----SLG-----NGREQSPD-RGV	608
	ZmANT1	142	QQRQD-----LLSSEAFSLHDIVS-VDAAGTGTGTGGM-----SNASSSLAPSVNSREQSPD-R--	196
	GhANT1	496	QQHQS-----TNTNDA-----SLAN-----SGSRNSNPNQSPK	524
g1244708	568	TN-----QSFVALDNMFHQVEE\$SKARTHV-----SNPSS-LATLSLSSGREGSPD-RTS	616	
	GmANT2	530	QKG-----FMGDAHSAHGIUGFVDESAADEIDVPGGKISGINFSN\$SS-LVTSLSNSREGGSPE-RLG	591
g1244708	500	-----LLSFPAIFALPQVQNMFGSN-----MGGNMS\$WTSN\$NAELK-TVALTLPQMPVFAA	551	
	GmANT1	612	SLL-FPMPPMETKIVNP-----IGTSVTSWLP\$PTVQMRPSP\$AISL\$HLPVFA\$	659
	OsANT2	609	GGGGGGVATLFAKPAASAKLYSPVP-----LNTWAS\$P\$AV\$SVPAR--AGV\$IAHLP\$FA\$	665
	ZmANT1	197	GGASLMLF-----AKPVAAPKLACPLP-----LGSWV\$P\$-AV\$SARPP-----GV\$IAHLPVFAA	246
	GhANT1	525	GISGLASDKFGIGGDY\$HHGYFSLKGSKYEDGNSETDN\$ENR\$NLGNLGLVHK-----TPMFA\$	582
g1244708	617	LPMLSGMPSTASKL-----ATPNPNVNSNDP\$PH--LRPALTLPQMPVFAA	661	
	GmANT2	592	LAML-----YAKHHPTAVSLA-----AMNPWMPMPAPAAAHV-MRPP\$IAHLPVFAA	638